AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1-26 (canceled)

27. (currently amended) A method of identifiably detecting a mismatch in any of a plurality of DNA duplexes of distinct nucleic acid sequence, comprising:

phenotypically sorting from said plurality of distinct duplexes those that initiate a mismatch corepair event in a bacterial cell, to form a phenotypically sorted population, wherein such mismatch repair event takes place only when there are together in a polynucleotide within the bacterial cell (i) a distinct duplex having a mismatch that activates a methyl-directed mismatch repair system of the bacterial cell, and (ii) an inactive marker having a mismatch of at least about 5 nucleotides in length that does not activate the methyl-directed mismatch repair system of the bacterial cell, and wherein such marker is repaired to generate a distinguishable cellular phenotype; and then

identifying the duplexes present in said phenotypically sorted population,

wherein identification is effected by identifying at least one genotypically detectable genetic element uniquely linked to each said phenotypically sorted duplex.

28. (original) The method of claim 27, wherein each of said at least one genotypically detectable genetic elements is a nucleic acid sequence tag, each of said sequence tags being unique among said plurality of sequence tags, and wherein said sorted duplexes are identified by specific hybridization of said sequence tags, tagged duplexes, or nucleic acids derived therefrom, to a microarray having probes complementary to said plurality of sequence tags.

29. (original) The method of claim 28, wherein each of said plurality of distinct sequence-tagged duplexes is itself further linked to at least one priming sequence, said at least one priming sequence being sufficient to allow enzymatic amplification of the tagged duplex linked thereto.

30. (original) The method of claim 28 or claim 29, wherein each of said sequence tags is at least 17 nucleotides in length.

31. (original) The method of claim 30, wherein each of said sequence tags is at least 20 nucleotides in length.

32. (original) The method of claim 31, wherein each of said sequence tags is at least 25 nucleotides in length.

33. (original) The method of claim 27, wherein at least one among said plurality of distinct DNA duplexes has at least one strand identical in sequence to a naturally-occurring genomic sequence.

34. (original) The method of claim 33, wherein each of said at least one duplexes having sequence identical to naturally-occurring genomic sequence is obtained by amplification from a genomic template.

35. (original) The method of claim 33 or claim 34, wherein said genomic sequence is a eukaryotic genomic sequence.

36. (original) The method of claim 35, wherein said eukaryotic genomic sequence is selected from the group consisting of: yeast genomic sequence, plant genomic sequence, and mammalian genomic sequence.

37. (original) The method of claim 36, wherein said eukaryotic genomic sequence is mammalian genomic sequence.

38. (original) The method of claim 37, wherein said mammalian genomic sequence is selected from the group consisting of: murine genomic sequence, rattus genomic sequence, and human genomic sequence.

39. (original) The method of claim 38, wherein said mammalian genomic sequence is human genomic sequence.

40. (original) The method of claim 33, wherein said plurality of distinct DNA duplexes includes at least two duplexes having the sequence of different allelic variants of a single genomic locus.

41. (original) The method of claim 40, wherein said plurality of distinct DNA duplexes includes at least three duplexes having the sequence of different allelic variants of a single genomic locus.

42. (original) The method of any one of claims 27, 33 or 40, wherein said plurality of distinct

DNA duplexes includes at least 10 distinct DNA duplexes.

43. (original) The method of claim 32, wherein said plurality of distinct DNA duplexes includes at least 100 distinct DNA duplexes.

44. (original) The method of claim 43, wherein said plurality of distinct DNA duplexes includes at least 1000 distinct DNA duplexes.

45. (original) The method of claim 44, wherein said plurality of distinct DNA duplexes includes at least 5000 distinct DNA duplexes.

46. (original) The method of claim 45, wherein said plurality of distinct DNA duplexes includes at least 10,000 distinct DNA duplexes.

47. (original) The method of claim 27, further comprising:

phenotypically sorting from said plurality of distinct duplexes those that are incapable of initiating a mismatch corepair event *in vivo*; and then

identifying duplexes present in said further phenotypically sorted population,

wherein said identifying is identification of at least one genotypically detectable genetic element uniquely linked to each said duplex.

48-55 (canceled)